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研究报告

浙江地区青霉素耐药肺炎链球菌PBPs基因及氨基酸序列研究

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摘要 为阐明温州地区青霉素耐药肺炎链球菌（PRSP）的青霉素结合蛋白（PBPs）的基因和氨基酸序列的变异特点，对温州医学院自2000年11月～2004年1月收集的26份肺炎链球菌进行分离、鉴定及青霉素药敏实验，并对每株链球菌的PBP1A、PBP2B、PBP2X基因进行PCR扩增和直接测序，通过序列比对与生物信息学分析。结果表明，研究中的PBP1A的主要突变位点是保守基序KTG之后的4个连续氨基酸替换Thr574Ala、Ser575Thr、Gln576Gly、Phe577Tyr和保守序列STMK内的氨基酸替换Thr371Ser；PBP2B的主要突变位点是保守序列SSN之后的氨基酸替换Thr451Ala；PBP2X的主要突变位点是保守基序STMK 内的氨基酸替换Thr338Ala。以上突变类型以及菌株的青霉素耐药水平与文献报道相符。研究检测的PRSP的PBPs基因中暂未发现本地区特有的（新的）基因突变，也未检测出文献报道的某些与青霉素抗性相关的氨基酸替换。

关键词 肺炎链球菌（SP）； 青霉素耐药的肺炎链球菌(PRSP)； 青霉素结合蛋白(PBPs)

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Study on PBPs Genes of Penicillin-resistant Streptococcus pneumonia in Zhejiang Province

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Abstract

To elucidate alternations in gene/amino acid sequence of penicillin-binding proteins (PBPs) 1A, 2B, 2X from clinical isolates of penicillin-resistant Streptococcus pneumonia (PRSP) in Zhejiang Province, 26 strains of Streptococcus pneumonia were collected from November 2001 to January 2004. The antibiotics susceptibility of these strains was detected. PCR amplification and direct sequencing of PBP1A, 2B, 2X genes were performed. The sequence variations of PBP genes of the PRSPs in this region were studied by sequence BLAST analysis. It was shown that the main alternations of PBP1A were the four consecutive amino acid substitutions (Thr574Ala, Ser575Thr, Gln576Gly, Phe577Tyr) following the conservative motif KTG and the amino acid substitution Thr371Ser in the conservative motif STMK. The main alternation of PBP2B was Thr451Ala following the conservative motif SSN，and the main alternation of PBP2X was Thr338Ala in conservative motif STMK. The above mutation sites and drug resistant level were consistent to the data reported previously. Neither new gene mutation specific to these strains nor certain amino acid substitutions related to penicillin resistance reported was identified in the genes.

Key words Streptococcus pneumonia（SP）； penicillin resistant Streptococcus pneumonia (PRSP)；penicillin-binding proteins(PBP)

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